

Dynamical Behavior of Networks and Cellular Automata

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Successful initial steps toward improved understanding of the dynamics of biological systems with network-style communications have been achieved. They will lead toward the ultimate objective of elucidation of some elements of the origin of life on Earth and perhaps elsewhere.

A novel data processing algorithm, which addresses the inverse problem of deducing internal network structure from behavior, as represented by time-series data on signals at one or more output nodes, has been developed. Data analysis techniques, based on information theory and Bayesian change-point determination methods (originally developed for astrophysical systems) are being applied to this reverse engineering of biological systems, as well as to automatic genetic sequence decoding.

Models of normal and neoplastic cell dynamics incorporate all relevant biochemical and physiological parameters and describe regulatory interactions in a deterministic manner. Because these realistic Boolean networks behave very much like actual biological systems, they aid in addressing a series of

essential questions in cancer biology and therapy. With some extensions, the same models describe the origin and development of primitive cellular life.

A program to study continuous-time networks, with time-delay factors, starts from known exact solutions to such systems when the interactions are linear. The nonlinear interactions, which characterize biological organisms, are being addressed with novel computational techniques developed especially for such networks.

All of this work is carried out in a context of modern information technology, including the use in the models of neural networks, genetic algorithms, and their combinations and extensions, and with the goal of incorporating new large-scale data acquisition efforts in the biotechnology industry and elsewhere.

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